

# Raw Sequence Listing Error Summary

SERIAL NUMBER: 09/254,870

## ERROR DETECTED SUGGESTED CORRECTION

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1        Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2        Wrapped Aminos      The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3        Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4        Misaligned Amino Acid Numbering      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5        Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6        Variable Length      Sequence(s)        contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7        PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s)       . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.
- 8        Skipped Sequences (OLD RULES)      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9        Skipped Sequences (NEW RULES)      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 10        Use of n's or Xaa's (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11        Use of <213>Organism (NEW RULES)      Sequence(s)        are missing this mandatory field or its response.
- 12        Use of <220>Feature (NEW RULES)      Sequence(s)        are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13        PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

RECEIVED  
JUL 28 2000  
TECH CENTER 1600/2800

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

*↑ move up - all responses must be on same line as heading*  
~~(A) NAME: Max-Planck-Gesellschaft zur Foerderung der Wissenschaften e.V.~~

~~(B) STREET: none~~

~~(C) CITY: Berlin~~

~~(E) COUNTRY: DE~~

~~(F) POSTAL CODE (ZIP): none~~

*↑*  
~~(A) NAME: CNRS~~

~~(B) STREET: rue de la cardonille~~

~~(C) CITY: Montpellier Cedex 05~~

~~(E) COUNTRY: FR~~

~~(F) POSTAL CODE (ZIP): 34094~~

(ii) TITLE OF INVENTION: Nucleic acid molecules coding for mammalian tumor suppressor proteins and methods for their isolation

(iii) NUMBER OF SEQUENCES: 17

(v) ~~(iv)~~ COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(vi) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE:

(B) STREET:

(C) CITY:

(D) STATE:

(E) COUNTRY:

(F) ZIP:

(vii) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

*add these mandatory headings for a U.S. case*

*insert these mandatory headings and responses for a U.S. case*

*FYI: EPO format of PatentIn is invalid for U.S. case*

C. Patterson

Does Not Comply  
Corrected Diskette Needed

1652

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/254,870

DATE: 07/12/2000  
TIME: 14:07:01

Input Set : A:\52130apctus.app.txt  
Output Set : N:\CRF3\07122000\I254870.raw

see last page  
↓

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:  
E--> 6 (i) APPLICANT:  
20 (ii) TITLE OF INVENTION: Nucleic acid molecules coding for mammalian  
21 tumor suppressor proteins and methods for their isolation  
23 (iii) NUMBER OF SEQUENCES: 17  
E--> 0 (iv) CORRESPONDENCE ADDRESS:  
15 (B) STREET: rue de la cardonille  
16 (C) CITY: Montpellier Cedex 05  
17 (E) COUNTRY: FR  
C--> 18 (F) ZIP: 34094  
C--> 25 (v) COMPUTER READABLE FORM:  
26 (A) MEDIUM TYPE: Floppy disk  
27 (B) COMPUTER: IBM PC compatible  
28 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
29 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
C--> 0 (vi) CURRENT APPLICATION DATA:  
C--> 0 (A) APPLICATION NUMBER: US/09/254,870  
C--> 0 (B) FILING DATE: 16-Aug-1999  
C--> 0 (viii) ATTORNEY/AGENT INFORMATION:  
14 (A) NAME: CNRS

ERRORED SEQUENCES

32 (2) INFORMATION FOR SEQ ID NO: 1:  
34 (i) SEQUENCE CHARACTERISTICS:  
35 (A) LENGTH: 2790 base pairs  
36 (B) TYPE: nucleic acid  
37 (C) STRANDEDNESS: single  
38 (D) TOPOLOGY: linear  
40 (ii) MOLECULE TYPE: cDNA to mRNA  
43 (ix) FEATURE:  
44 (A) NAME/KEY: CDS  
45 (B) LOCATION: 542..2545  
48 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
E--> 50 GAATTCGGGA GAGCAAGCGG GCATCTCCTG GCGGCCGTCA TGGCTGCTTA  
51 GGCTGCGCTG 60  
E--> 53 CCGCGGATC GCGGATCCGG GATCGGAGAT CTGACGGCGA CGCCTGAGTC  
54 CCGCTAGGGT 120  
E--> 56 AGGTCTGGGT TGGAGTCTGT GCCTGCTTCC TTGGCGTGTG GTTGTTCCTG  
57 CTTGATTGCT 180  
E--> 59 TCAGCGTGCC ATCGGCTTCG TATTGCATA GGAGTCAGAG GAGTTAATCT  
60 TGTCTCCTCG 240  
E--> 62 AAGATAGACT CTCATGGTTT ATGATCCATC TCTGTGAGAA GACTTTATTT  
63 GTCTGTCTCT 300  
E--> 65 TCTCACAGGT TTGAGTCTTC AGACTTCTAC AGAACTCCAT AATATCTGCC

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60 format error -  
120  
↓ see item 1  
an error  
summary  
sheet

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/254,870

DATE: 07/12/2000  
TIME: 14:07:01

Input Set : A:\52130apctus.app.txt  
Output Set : N:\CRF3\07122000\I254870.raw

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66 TCACAGCTGG      360
E--> 68 CTTTCCTGCT CTCACAGAAG ATACCCAGCT ATTGTGCTCT GGATCTCTCC
69 TGGCTGCTAG      420
E--> 71 GCTGTAGCGC TGCCTTTCTG GAGTCAGGCT GTAGTGACTC CCCACCTTCT
72 TTCTGTCTGG      480
E--> 74 GCTTAAATGG CACAGCAGTT CCTCAGCACA TCTGAAGAAG AAAGTGTGAG
75 AACCAAAGGC      540
77 C ATG GCT CCA TTC CGC TGT CAA AAA TGT GGC AAG TCC TTC GTC ACC
78 Met Ala Pro Phe Arg Cys Gln Lys Cys Gly Lys Ser Phe Val Thr
79      1          5          10          15
E--> 81 CTG GAG AAG TTC ACC ATT CAC AAT TAT TCC CAC TCC AGG GAG CGC CCA
W--> 82 634
83 Leu Glu Lys Phe Thr Ile His Asn Tyr Ser His Ser Arg Glu Arg Pro
W--> 84      20          25          30
E--> 86 TTC AAG TGC TCG AAG GCT GAG TGT GGC AAA GCC TTC GTC TCC AAG TAT
W--> 87 682
88 Phe Lys Cys Ser Lys Ala Glu Cys Gly Lys Ala Phe Val Ser Lys Tyr
W--> 89      35          40          45
E--> 91 AAG CTG ATG AGA CAC ATG GCC ACA CAC TCG CCA CAG AAG ATT CAC CAG
W--> 92 730
93 Lys Leu Met Arg His Met Ala Thr His Ser Pro Gln Lys Ile His Gln
W--> 94      50          55          60
E--> 96 TGT ACT CAC TGT GAG AAG ACA TTC AAC CGG AAG GAC CAC CTG AAG AAC
W--> 97 778
98 Cys Thr His Cys Glu Lys Thr Phe Asn Arg Lys Asp His Leu Lys Asn
W--> 99      65          70          75
E--> 101 CAC CTC CAG ACC CAC GAT CCC AAC AAG ATC TCC TAC GCG TGT GAC GAT
W--> 102 826
103 His Leu Gln Thr His Asp Pro Asn Lys Ile Ser Tyr Ala Cys Asp Asp
W--> 104 80      85          90          95
E--> 106 TGC GGC AAG AAG TAC CAC ACC ATG CTG GGC TAC AAG AGG CAC CTG GCC
W--> 107 874
108 Cys Gly Lys Lys Tyr His Thr Met Leu Gly Tyr Lys Arg His Leu Ala
W--> 109      100          105          110
E--> 111 CTG CAC TCG GCG AGC AAT GGC GAT CTC ACC TGT GGG GTG TGC ACC CTG
W--> 112 922
113 Leu His Ser Ala Ser Asn Gly Asp Leu Thr Cys Gly Val Cys Thr Leu
W--> 114      115          120          125
E--> 116 GAG CTG GGG AGC ACC GAG GTC CTG CTG GAC CAC CTC AAG TCT CAC GCG
W--> 117 970
118 Glu Leu Gly Ser Thr Glu Val Leu Leu Asp His Leu Lys Ser His Ala
W--> 119      130          135          140
E--> 121 GAA GAA AAG GCC AAC CAG GCA CCC AGG GAG AAG AAA TAC CAG TGC GAC
W--> 122 1018
123 Glu Glu Lys Ala Asn Gln Ala Pro Arg Glu Lys Lys Tyr Gln Cys Asp
W--> 124      145          150          155
E--> 126 CAC TGT GAT AGA TGC TTC TAC ACC CGG AAA GAT GTG CGT CGC CAC CTG
W--> 127 1066
128 His Cys Asp Arg Cys Phe Tyr Thr Arg Lys Asp Val Arg Arg His Leu

```

586

*same*  
↓

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/254,870

DATE: 07/12/2000  
 TIME: 14:07:01

Input Set : A:\52130apctus.app.txt  
 Output Set: N:\CRF3\07122000\I254870.raw

W--> 129 160 165 170 175  
 E--> 131 GTG GTC CAC ACA GGA TGC AAG GAC TTC CTG TGT CAG TTC TGT GCC CAG  
 W--> 132 1114  
 133 Val Val His Thr Gly Cys Lys Asp Phe Leu Cys Gln Phe Cys Ala Gln  
 W--> 134 180 185 190  
 E--> 136 AGA TTT GGG CGC AAA GAC CAC CTC ACT CGT CAC ACC AAG AAG ACC CAC  
 W--> 137 1162  
 138 Arg Phe Gly Arg Lys Asp His Leu Thr Arg His Thr Lys Lys Thr His  
 W--> 139 195 200 205  
 E--> 141 TCC CAG GAG CTG ATG CAA GAG AAT ATG CAG GCA GGA GAT TAC CAG AGC  
 W--> 142 1210  
 143 Ser Gln Glu Leu Met Gln Glu Asn Met Gln Ala Gly Asp Tyr Gln Ser  
 W--> 144 210 215 220  
 E--> 147 AAT TTC CAA CTC ATT GCG CCT TCA ACT TCG TTC CAG ATA AAG GTT GAT  
 W--> 148 1258  
 149 Asn Phe Gln Leu Ile Ala Pro Ser Thr Ser Phe Gln Ile Lys Val Asp  
 W--> 150 225 230 235  
 E--> 152 CCC ATG CCT CCT TTC CAG CTA GGA GCG GCT CCC GAG AAC GGG CTT GAT  
 W--> 153 1306  
 154 Pro Met Pro Pro Phe Gln Leu Gly Ala Ala Pro Glu Asn Gly Leu Asp  
 W--> 155 240 245 250 255  
 E--> 157 GGT GGC TTG CCA CCC GAG GTT CAT GGT CTA GTG CTT GCT GCC CCA GAA  
 W--> 158 1354  
 159 Gly Gly Leu Pro Pro Glu Val His Gly Leu Val Leu Ala Ala Pro Glu  
 W--> 160 260 265 270  
 E--> 162 GAA GCT CCC CAA CCC ATG CCG CCC TTG GAG CCT TTG GAG CCT TTG GAG  
 W--> 163 1402  
 164 Glu Ala Pro Gln Pro Met Pro Pro Leu Glu Pro Leu Glu Pro Leu Glu  
 W--> 165 275 280 285  
 E--> 167 CCT TTG GAG CCT TTG GAG CCG ATG CAG TCT TTG GAG CCT TTG CAG CCT  
 W--> 168 1450  
 169 Pro Leu Glu Pro Leu Glu Pro Met Gln Ser Leu Glu Pro Leu Gln Pro  
 W--> 170 290 295 300  
 E--> 172 TTG GAG CCG ATG CAG CCT TTG GAG CCA ATG CAG CCT TTG GAG CCG ATG  
 W--> 173 1498  
 174 Leu Glu Pro Met Gln Pro Leu Glu Pro Met Gln Pro Leu Glu Pro Met  
 W--> 175 305 310 315  
 E--> 177 CAG CCT TTA GAG CCT TTG GAG CCT CTG GAG CCG ATG CAG CCT TTG GAG  
 W--> 178 1546  
 179 Gln Pro Leu Glu Pro Leu Glu Pro Leu Glu Pro Met Gln Pro Leu Glu  
 W--> 180 320 325 330 335  
 E--> 182 CCG ATG CAG CCT TTG GAG CCT ATG CAG CCA ATG CTG CCA ATG CAG CCA  
 W--> 183 1594  
 184 Pro Met Gln Pro Leu Glu Pro Met Gln Pro Met Leu Pro Met Gln Pro  
 W--> 185 340 345 350  
 E--> 187 ATG CAG CCA ATG CAG CCA ATG CAG CCA ATG CTG CCA ATG CAG CCA ATG  
 W--> 188 1642  
 189 Met Gln Pro Met Gln Pro Met Gln Pro Met Leu Pro Met Gln Pro Met  
 W--> 190 355 360 365

*same*

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PATENT APPLICATION: US/09/254,870

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TIME: 14:07:01

Input Set : A:\52130apctus.app.txt  
Output Set: N:\CRF3\07122000\I254870.raw

E--> 192 CTG CCA ATG CAG CCA ATG CAG CCA ATG CAG CCA ATG CTG CCA ATG CCA  
W--> 193 1690  
194 Leu Pro Met Gln Pro Met Gln Pro Met Gln Pro Met Leu Pro Met Pro  
W--> 195 370 375 380  
E--> 197 GAG CCG TCT TTC ACT CTG CAC CCT GGC GTA GTT CCC ACC TCT CCT CCC  
W--> 198 1738  
199 Glu Pro Ser Phe Thr Leu His Pro Gly Val Val Pro Thr Ser Pro Pro  
W--> 200 385 390 395  
E--> 202 CCA ATT ATT CTT CAG GAG CAT AAG TAT AAT CCT GTT CCT ACC TCA TAT  
W--> 203 1786  
204 Pro Ile Ile Leu Gln Glu His Lys Tyr Asn Pro Val Pro Thr Ser Tyr  
W--> 205 400 405 410 415  
E--> 207 GCC CCA TTT GTA GGC ATG CCC GTC AAA CCA GAT GGC AAG GCC TTT TGC  
W--> 208 1834  
209 Ala Pro Phe Val Gly Met Pro Val Lys Ala Asp Gly Lys Ala Phe Cys  
W--> 210 420 425 430  
E--> 212 AAC GTG GGT TTC TTT GAG GAA TTT CCT CTG CAA GAG CCT CAG GCG CCT  
W--> 213 1882  
214 Asn Val Gly Phe Phe Glu Glu Phe Pro Leu Gln Glu Pro Gln Ala Pro  
W--> 215 435 440 445  
E--> 217 CTC AAG TTC AAC CCA TGT TTT GAG ATG CCT ATG GAG GGG TTT GGG AAA  
W--> 218 1930  
219 Leu Lys Phe Asn Pro Cys Phe Glu Met Pro Met Glu Gly Phe Gly Lys  
W--> 220 450 455 460  
E--> 223 GTC ACC CTG TCC AAA GAG CTG CTG GTA GAT GCT GTG AAT ATA GCC ATT  
W--> 224 1978  
225 Val Thr Leu Ser Lys Glu Leu Leu Val Asp Ala Val Asn Ile Ala Ile  
W--> 226 465 470 475  
E--> 228 CCT GCC TCT CTG GAG ATT TCC TCC CTA TTG GGG TTT TGG CAG CTC CCC  
W--> 229 2026  
230 Pro Ala Ser Leu Glu Ile Ser Ser Leu Leu Gly Phe Trp Gln Leu Pro  
W--> 231 480 485 490 495  
E--> 233 CCT CCT ACT CCC CAG AAT GGC TTT GTG AAT AGC ACC ATC CCT GTG GGG  
W--> 234 2074  
235 Pro Pro Thr Pro Gln Asn Gly Phe Val Asn Ser Thr Ile Pro Val Gly  
W--> 236 500 505 510  
E--> 238 CCT GGG GAG CCA CTG CCC CAT AGG ATA ACC TGT CTG GCG CAG CAG CAG  
W--> 239 2122  
240 Pro Gly Glu Pro Leu Pro His Arg Ile Thr Cys Leu Ala Gln Gln Gln  
W--> 241 515 520 525  
E--> 243 CCA CCG CCA CTG CCG CCG CCA CCA CCG CTG CCA CTG CCA CAG CCA CTG  
W--> 244 2170  
245 Pro Pro Pro Leu Pro Pro Pro Pro Pro Leu Pro Leu Pro Gln Pro Leu  
W--> 246 530 535 540  
E--> 248 CCA GTG CCA CAG CCA CTA CCA CAG CCA CAG ATG CAG CCA CAG TTT CAG  
W--> 249 2218  
250 Pro Val Pro Gln Pro Leu Pro Gln Pro Gln Met Gln Pro Gln Phe Gln  
W--> 251 545 550 555  
E--> 253 TTG CAG ATC CAG CCC CAG ATG CAG CTA CCA CAG CTG CTG CCG CAA CTG

*same*

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PATENT APPLICATION: US/09/254,870

DATE: 07/12/2000  
TIME: 14:07:01

Input Set : A:\52130apctus.app.txt  
Output Set: N:\CRF3\07122000\I254870.raw

W--> 254 2266  
255 Leu Gln Ile Gln Pro Gln Met Gln Leu Pro Gln Leu Leu Pro Gln Leu 575  
W--> 256 560 565 570  
E--> 258 CAA CCT CAG CAG CAG CCT GAT CCT GAG CCA GAG CCA GAG CCA GAG CCA  
W--> 259 2314  
260 Gln Pro Gln Gln Gln Pro Asp Pro Glu Pro Glu Pro Glu Pro Glu Pro 590  
W--> 261 580 585  
E--> 263 GAG CCA GAG CCA GAG CCA GAG CCG GAA CCG GAA CCG GAG CCA GAG CCA  
W--> 264 2362  
265 Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro 605  
W--> 266 595 600  
E--> 268 GAG CCA GAA CCA GAG CCA GAG GAA GAA CAG GAA GAG CCA GAA GAA GAG  
W--> 269 2410  
270 Glu Pro Glu Pro Glu Pro Glu Glu Glu Gln Glu Glu Ala Glu Glu Glu 620  
W--> 271 610 615  
E--> 273 GCA GAG GAA GGA GCA GAG GAA GGA GCA GAA CCA GAG CCA CAG GCA GAA  
W--> 274 2458  
275 Ala Glu Glu Gly Ala Glu Glu Gly Ala Glu Pro Glu Ala Gln Ala Glu 635  
W--> 276 625 630  
E--> 278 GAA GAG GAA GAG GAA GAG GAA GCG GAA GAG CCA CAG CCA GAA GAA GCC  
W--> 279 2506  
280 Glu Glu Glu Glu Glu Glu Glu Ala Glu Glu Pro Gln Pro Glu Glu Ala 655  
W--> 281 640 645  
E--> 283 CAA ATA GCA GGA CTC GTC TAT AAG AAA TGG ACA GTT TAG TTCCTCTCT  
W--> 284 2555  
285 Gln Ile Ala Gly Leu Val Tyr Lys Lys Trp Thr Val \* 665  
W--> 286 660  
E--> 288 TGTTAGCTTA CTCTGTAGTT TCTTCTTCTT GTTGCCCATTT GTGTAGCTTT  
289 ATAGAGTGTG 2615  
E--> 291 ACGCTATTGA TGCTCTCCATT TTTTAAAGTG AATTTAAATG TACTGTTCAA  
292 TATTTTTCAT 2675  
E--> 294 CTGATGTTGT TCCAATGTGA GTTACGACTT CATTTATCTT AAAGACAAAA  
295 CTGGTTGTCA 2735  
E--> 297 GTCATATCTG ACAGAAGAAA GAAATCACTG TGTAACCAAG CCATATAGCG  
298 GCCGC 2790  
302 (2) INFORMATION FOR SEQ ID NO: 2:  
304 (i) SEQUENCE CHARACTERISTICS:  
305 (A) LENGTH: 666 amino acids  
306 (B) TYPE: amino acid  
307 (D) TOPOLOGY: linear  
309 (ii) MOLECULE TYPE: protein  
310 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
312 Met Ala Pro Phe Arg Cys Gln Lys Cys Gly Lys Ser Phe Val Thr Leu 15  
313 1 5 10  
315 Glu Lys Phe Thr Ile His Asn Tyr Ser His Ser Arg Glu Arg Pro Phe 30  
316 20 25  
318 Lys Cys Ser Lys Ala Glu Cys Gly Lys Ala Phe Val Ser Lys Tyr Lys 45  
319 35 40  
321 Leu Met Arg His Met Ala Thr His Ser Pro Gln Lys Ile His Gln Cys

*same*

667 (p. 7)

RAW SEQUENCE LISTING  
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 TIME: 14:07:01

Input Set : A:\52130apctus.app.txt  
 Output Set: N:\CRF3\07122000\I254870.raw

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322      50      55      60
324 Thr His Cys Glu Lys Thr Phe Asn Arg Lys Asp His Leu Lys Asn His
325 65      70      75      80
327 Leu Gln Thr His Asp Pro Asn Lys Ile Ser Tyr Ala Cys Asp Asp Cys
328      85      90      95
330 Gly Lys Lys Tyr His Thr Met Leu Gly Tyr Lys Arg His Leu Ala Leu
331      100      105      110
333 His Ser Ala Ser Asn Gly Asp Leu Thr Cys Gly Val Cys Thr Leu Glu
334      115      120      125
336 Leu Gly Ser Thr Glu Val Leu Leu Asp His Leu Lys Ser His Ala Glu
337      130      135      140
339 Glu Lys Ala Asn Gln Ala Pro Arg Glu Lys Lys Tyr Gln Cys Asp His
340 145      150      155      160
342 Cys Asp Arg Cys Phe Tyr Thr Arg Lys Asp Val Arg Arg His Leu Val
343      165      170      175
345 Val His Thr Gly Cys Lys Asp Phe Leu Cys Gln Phe Cys Ala Gln Arg
346      180      185      190
348 Phe Gly Arg Lys Asp His Leu Thr Arg His Thr Lys Lys Thr His Ser
349      195      200      205
351 Gln Glu Leu Met Gln Glu Asn Met Gln Ala Gly Asp Tyr Gln Ser Asn
352      210      215      220
354 Phe Gln Leu Ile Ala Pro Ser Thr Ser Phe Gln Ile Lys Val Asp Pro
355 225      230      235      240
357 Met Pro Pro Phe Gln Leu Gly Ala Ala Pro Glu Asn Gly Leu Asp Gly
358      245      250      255
360 Gly Leu Pro Pro Glu Val His Gly Leu Val Leu Ala Ala Pro Glu Glu
361      260      265      270
364 Ala Pro Gln Pro Met Pro Pro Leu Glu Pro Leu Glu Pro Leu Glu Pro
365      275      280      285
367 Leu Glu Pro Leu Glu Pro Met Gln Ser Leu Glu Pro Leu Gln Pro Leu
368      290      295      300
370 Glu Pro Met Gln Pro Leu Glu Pro Met Gln Pro Leu Glu Pro Met Gln
371 305      310      315      320
373 Pro Leu Glu Pro Leu Glu Pro Leu Glu Pro Met Gln Pro Leu Glu Pro
374      325      330      335
376 Met Gln Pro Leu Glu Pro Met Gln Pro Met Leu Pro Met Gln Pro Met
377      340      345      350
379 Gln Pro Met Gln Pro Met Gln Pro Met Leu Pro Met Gln Pro Met Leu
380      355      360      365
382 Pro Met Gln Pro Met Gln Pro Met Gln Pro Met Leu Pro Met Pro Glu
383      370      375      380
385 Pro Ser Phe Thr Leu His Pro Gly Val Val Pro Thr Ser Pro Pro Pro
386 385      390      395      400
388 Ile Ile Leu Gln Glu His Lys Tyr Asn Pro Val Pro Thr Ser Tyr Ala
389      405      410      415
391 Pro Phe Val Gly Met Pro Val Lys Ala Asp Gly Lys Ala Phe Cys Asn
392      420      425      430
394 Val Gly Phe Phe Glu Glu Phe Pro Leu Gln Glu Pro Gln Ala Pro Leu
395      435      440      445

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Input Set : A:\52130apctus.app.txt  
Output Set: N:\CRF3\07122000\I254870.raw

```

397 Lys Phe Asn Pro Cys Phe Glu Met Pro Met Glu Gly Phe Gly Lys Val
398      450      455      460
400 Thr Leu Ser Lys Glu Leu Leu Val Asp Ala Val Asn Ile Ala Ile Pro
401 465      470      475      480
403 Ala Ser Leu Glu Ile Ser Ser Leu Leu Gly Phe Trp Gln Leu Pro Pro
404      485      490      495
406 Pro Thr Pro Gln Asn Gly Phe Val Asn Ser Thr Ile Pro Val Gly Pro
407      500      505      510
409 Gly Glu Pro Leu Pro His Arg Ile Thr Cys Leu Ala Gln Gln Gln Pro
410      515      520      525
412 Pro Pro Leu Pro Pro Pro Pro Pro Leu Pro Leu Pro Gln Pro Leu Pro
413      530      535      540
415 Val Pro Gln Pro Leu Pro Gln Pro Gln Met Gln Pro Gln Phe Gln Leu
416 545      550      555      560
418 Gln Ile Gln Pro Gln Met Gln Leu Pro Gln Leu Leu Pro Gln Leu Gln
419      565      570      575
421 Pro Gln Gln Gln Pro Asp Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu
422      580      585      590
424 Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu
425      595      600      605
427 Pro Glu Pro Glu Pro Glu Glu Gln Glu Glu Ala Glu Glu Glu Ala
428      610      615      620
430 Glu Glu Gly Ala Glu Glu Gly Ala Glu Pro Glu Ala Gln Ala Glu Glu
431 625      630      635      640
433 Glu Glu Glu Glu Glu Glu Ala Glu Glu Pro Gln Pro Glu Glu Ala Gln
434      645      650      655
E--> 436 Ile Ala Gly Leu Val Tyr Lys Lys Trp Thr Val
437      660      665
680 (2) INFORMATION FOR SEQ ID NO: 16:
682 (i) SEQUENCE CHARACTERISTICS:
683 (A) LENGTH: 2334 base pairs
684 (B) TYPE: nucleic acid
685 (C) STRANDEDNESS: single
686 (D) TOPOLOGY: linear
688 (ii) MOLECULE TYPE: cDNA
690 (iii) HYPOTHETICAL: NO
693 (ix) FEATURE:
694 (A) NAME/KEY: CDS
695 (B) LOCATION: 803..2192
699 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:
E--> 701 CCGTTCTTTC AATTCAGAAT TTGTTTATAG TTCTGTTATT GCATAGATTT
702 GCATACCTGT 60
E--> 704 TTTATGGTAT TTTAATACTG TTGGTTTAA AAAATACCAT TTCCTCTGAG
705 TGCTGTTCTG 120
E--> 707 AATATATTAT GTAAGCAATT TTGTGTGTTC TTTTTCCTCC ACTTGCAATA
708 AGCAGGGGAA 180
E--> 710 AAGTTGAGAG TTTTCTTAA TCCAGTCCCA AGTAGGACAA AGGATATGAG
711 TGTTTAAAGA 240
E--> 713 TCATCTATTA AAATGCATGA AAAAACAATA GAAATCTCC TGTGCACATC

```

*\* delete ending stop codon*

*format error  
see Item 1  
on Error Summary Sheet*

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/254,870

DATE: 07/12/2000  
 TIME: 14:07:01

Input Set : A:\52130apctus.app.txt  
 Output Set : N:\CRF3\07122000\I254870.raw

```

714 GCCAGTCGTTG      300
E--> 716 TGTGTGCTCT AGAAGTGAAG TTCAGGGGGT AACATAATGG AGGAATGTTT
717 TCCTAGCTTC      360
E--> 719 ATTCCTGAC GATGTACAAG GTCTCTTCTC ACAGGTTTGA ATCTTCAGAC
720 AACTTCTGG      420
E--> 722 GAGGACTGGG AGGACTCGGT CCCTGCCTCG CAGCAGATGT TCCCTGTCAC
723 TCAGTAGCCA      480
E--> 725 ATCCGGGGGA CCCAGGACAT GCCCCAGCTA TAGTGATGCA GATTACCTTT
726 CTGGTCCTGA      540
E--> 728 ATCGCACCTG TGCCTCGAGA CTTTCTCCCC TCAGCTTGAG ACTGCATGTA
729 AACTGGGATG      600
E--> 731 TGTGAAAGCA GGAAGCAAAG CTAGTGACAG CTGAGAGGTC CATGCTGCGG
732 TAGAACCAGG      660
E--> 734 CCCACGATGC TGCCTCTCCC GTGGTCTGGA GTTCAGTGC AGGGACTCTG
735 CTGATTGGCC      720
E--> 737 CAGCACCATC GTTCTGTTTG TGCTTAAATG GCACAGCATT TGGTCAGCAC
738 ATCTGAAAAG      780
E--> 740 GAAGGTGTGA GAAGCAAAGC CC ATG GCC ACG TTC CCC TGC CAG TTA TGT GGC
W--> 741      832
742 Met Ala Thr Phe Pro Cys Gln Leu Cys Gly
743      1      5      10
E--> 745 AAG ACG TTC CTC ACC CTG GAG AAG TTC ACG ATT CAC AAT TAT TCC CAC
W--> 746 880
747 Lys Thr Phe Leu Thr Leu Glu Lys Phe Thr Ile His Asn Tyr Ser His
W--> 748      15      20      25
E--> 750 TCC AGG GAG CGG CCG TAC AAG TGT GTG CAG CCT GAC TGT GGC AAA GCC
W--> 751 928
752 Ser Arg Glu Arg Pro Tyr Lys Cys Val Gln Pro Asp Cys Gly Lys Ala
W--> 753      30      35      40
E--> 755 TTT GTT TCC AGA TAT AAA TTG ATG AGG CAT ATG GCT ACC CAT TCT CCC
W--> 756 976
757 Phe Val Ser Arg Tyr Lys Leu Met Arg His Met Ala Thr His Ser Pro
W--> 758      45      50      55
E--> 760 CAG AAA TCT CAC CAG TGT GCT CAC TGT GAG AAG ACG TTC AAC CGG AAA
W--> 761 1024
762 Gln Lys Ser His Gln Cys Ala His Cys Glu Lys Thr Phe Asn Arg Lys
W--> 763      60      65      70
E--> 765 GAC CAC CTG AAA AAC CAC CTC CAG ACC CAC GAC CCC AAC AAA ATG GCC
W--> 766 1072
767 Asp His Leu Lys Asn His Leu Gln Thr His Asp Pro Asn Lys Met Ala
W--> 768      75      80      85      90
E--> 770 TTT GGG TGT GAG GAG TGT GGG AAG AAG TAC AAC ACC ATG CTG GGC TAT
W--> 771 1120
772 Phe Gly Cys Glu Glu Cys Gly Lys Lys Tyr Asn Thr Met Leu Gly Tyr
W--> 773      95      100      105
E--> 775 AAG AGG CAC CTG GCC CTC CAT GCG GCC AGC AGT GGG GAC CTC ACC TGT
W--> 776 1168
777 Lys Arg His Leu Ala Leu His Ala Ala Ser Ser Gly Asp Leu Thr Cys
W--> 778      110      115      120

```

*Same*

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/254,870

DATE: 07/12/2000  
 TIME: 14:07:01

Input Set : A:\52130apctus.app.txt  
 Output Set: N:\CRF3\07122000\I254870.raw

E--> 780 GGG GTC TGT GCC CTG GAG CTA GGG AGC ACC GAG GTG CTA CTG GAC CAC  
 W--> 781 1216  
 782 Gly Val Cys Ala Leu Glu Leu Gly Ser Thr Glu Val Leu Leu Asp His  
 W--> 783 125 130 135  
 E--> 785 CTC AAA GCC CAT GCG GAA GAG AAG CCC CCT AGC GGA ACC AAG GAA AAG  
 W--> 786 1264  
 787 Leu Lys Ala His Ala Glu Glu Lys Pro Pro Ser Gly Thr Lys Glu Lys  
 W--> 788 140 145 150  
 E--> 790 AAG CAC CAG TGC GAC CAC TGT GAA AGA TGC TTC TAC ACC CGG AAG GAT  
 W--> 791 1312  
 792 Lys His Gln Cys Asp His Cys Glu Arg Cys Phe Tyr Thr Arg Lys Asp  
 W--> 793 155 160 165 170  
 E--> 795 GTG CGA CGC CAC CTG GTG GTC CAC ACA GGA TGC AAG GAC TTC CTG TGC  
 W--> 796 1360  
 797 Val Arg Arg His Leu Val Val His Thr Gly Cys Lys Asp Phe Leu Cys  
 W--> 798 175 180 185  
 E--> 800 CAG TTC TGT GCC CAG AGA TTT GGG CGC AAG GAT CAC CTC ACC CGG CAT  
 W--> 801 1408  
 802 Gln Phe Cys Ala Gln Arg Phe Gly Arg Lys Asp His Leu Thr Arg His  
 W--> 803 190 195 200  
 E--> 805 ACC AAG AAG ACC CAC TCA CAG GAG CTG ATG AAA GAG AGC TTG CAG ACC  
 W--> 806 1456  
 807 Thr Lys Lys Thr His Ser Gln Glu Leu Met Lys Glu Ser Leu Gln Thr  
 W--> 808 205 210 215  
 E--> 810 GGA GAC CTT CTG AGC ACC TTC CAC ACC ATC TCG CCT TCA TTC CAA CTG  
 W--> 811 1504  
 812 Gly Asp Leu Leu Ser Thr Phe His Thr Ile Ser Pro Ser Phe Gln Leu  
 W--> 813 220 225 230  
 E--> 815 AAG GCT GCT GCC TTG CCT CCT TTC CCT TTA GGA GCT TCT GCC CAG AAC  
 W--> 816 1552  
 817 Lys Ala Ala Ala Leu Pro Pro Phe Pro Leu Gly Ala Ser Ala Gln Asn  
 W--> 818 235 240 245 250  
 E--> 820 GGG CTT GCA AGT AGC TTG CCA GCT GAG GTC CAT AGC CTC ACC CTC AGT  
 W--> 821 1600  
 822 Gly Leu Ala Ser Ser Leu Pro Ala Glu Val His Ser Leu Thr Leu Ser  
 W--> 823 255 260 265  
 E--> 825 CCC CCA GAA CAA GCC GCC CAG CCT ATG CAG CCG CTG CCA GAG TCC CTG  
 W--> 826 1648  
 827 Pro Pro Glu Gln Ala Ala Gln Pro Met Gln Pro Leu Pro Glu Ser Leu  
 W--> 828 270 275 280  
 E--> 830 GCC TCC CTC CAC CCC TCG GTA TCC CCT GGC TCT CCT CCG CCA CCC CTT  
 W--> 831 1696  
 832 Ala Ser Leu His Pro Ser Val Ser Pro Gly Ser Pro Pro Pro Pro Leu  
 W--> 833 285 290 295  
 E--> 835 CCC AAT CAC AAG TAC AAC ACC ACT TCT ACC TCA TAC TCC CCA CTT GCA  
 W--> 836 1744  
 837 Pro Asn His Lys Tyr Asn Thr Thr Ser Thr Ser Tyr Ser Pro Leu Ala  
 W--> 838 300 305 310  
 E--> 840 AGC CTG CCC CTC AAA GCA GAT ACT AAA GGT TTT TGC AAT ATC AGT TTG

*same*

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/254,870

DATE: 07/12/2000  
TIME: 14:07:01

Input Set : A:\52130apctus.app.txt  
Output Set: N:\CRF3\07122000\I254870.raw

W--> 841 1792  
842 Ser Leu Pro Leu Lys Ala Asp Thr Lys Gly Phe Cys Asn Ile Ser Leu 330  
W--> 843 315 320 325  
E--> 845 TTT GAG GAC TTG CCT CTG CAA GAG CCT CAG TCA CCT CAA AAG CTC AAC  
W--> 846 1840  
847 Phe Glu Asp Leu Pro Leu Gln Glu Pro Gln Ser Pro Gln Lys Leu Asn 345  
W--> 848 335 340  
E--> 850 CCA GGT TTT GAT CTG GCT AAG GGA AAT GCT GGT AAA GTA AAC CTG CCC  
W--> 851 1888  
852 Pro Gly Phe Asp Leu Ala Lys Gly Asn Ala Gly Lys Val Asn Leu Pro 360  
W--> 853 350 355  
E--> 855 AAG GAG CTG CCT GCA GAT GCT GTG AAC CTA ACA ATA CCT GCC TCT CTG  
W--> 856 1936  
857 Lys Glu Leu Pro Ala Asp Ala Val Asn Leu Thr Ile Pro Ala Ser Leu 375  
W--> 858 365 370  
E--> 860 GAC CTG TCC CCC CTG TTG GGC TTC TGG CAG CTG CCC CCT CCT GCT ACC  
W--> 861 1984  
862 Asp Leu Ser Pro Leu Leu Gly Phe Trp Gln Leu Pro Pro Pro Ala Thr 390  
W--> 863 380 385  
E--> 865 CAA AAT ACC TTT GGG AAT AGC ACT CTT GCC CTG GGG CCT GGG GAA TCT  
W--> 866 2032  
867 Gln Asn Thr Phe Gly Asn Ser Thr Leu Ala Leu Gly Pro Gly Glu Ser 410  
W--> 868 395 400 405  
E--> 870 TTG CCC CAC AGG TTA AGC TGT CTG GGG CAG CAG CAG CAA GAA CCC CCA  
W--> 871 2080  
872 Leu Pro His Arg Leu Ser Cys Leu Gly Gln Gln Gln Gln Glu Pro Pro 425  
W--> 873 415 420  
E--> 875 CTT GCC ATG GGC ACT GTG AGC CTG GGC CAG CTC CCC CTG CCC CCC ATC  
W--> 876 2128  
877 Leu Ala Met Gly Thr Val Ser Leu Gly Gln Leu Pro Leu Pro Pro Ile 440  
W--> 878 430 435  
E--> 880 CCT CAT GTG TTC TCA GCT GGC ACT GGC TCT GCC ATC CTG CCT CAT TTC  
W--> 881 2176  
882 Pro His Val Phe Ser Ala Gly Thr Gly Ser Ala Ile Leu Pro His Phe 455  
W--> 883 445  
885 CAT CAT GCA TTC AGA T AATTGATTTT TAAAGTGTAT TTTTCGTATT  
886 His His Ala Phe Arg  
W--> 887 460  
E--> 889 CTGGAAGATG TTTTAAGAAG CATTTTAAAT GTCAGTTACA ATATGAGAAA  
890 GATTTGGAAG 2282  
E--> 892 ACGAGACTGG GACTATGGCT TATTCAGTGA TGACTGGCTT GAGATGATAA GA  
W--> 893 2334  
897 (2) INFORMATION FOR SEQ ID NO: 17:  
899 (i) SEQUENCE CHARACTERISTICS:  
900 (A) LENGTH: 463 amino acids  
901 (B) TYPE: amino acid  
902 (D) TOPOLOGY: linear  
904 (ii) MOLECULE TYPE: protein  
905 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

2222

P.12

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/254,870

DATE: 07/12/2000  
 TIME: 14:07:01

Input Set : A:\52130apctus.app.txt  
 Output Set: N:\CRF3\07122000\I254870.raw

```

907 Met Ala Thr Phe Pro Cys Gln Leu Cys Gly Lys Thr Phe Leu Thr Leu
908 1 5 10 15
910 Glu Lys Phe Thr Ile His Asn Tyr Ser His Ser Arg Glu Arg Pro Tyr
911 20 25 30
913 Lys Cys Val Gln Pro Asp Cys Gly Lys Ala Phe Val Ser Arg Tyr Lys
914 35 40 45
916 Leu Met Arg His Met Ala Thr His Ser Pro Gln Lys Ser His Gln Cys
917 50 55 60
919 Ala His Cys Glu Lys Thr Phe Asn Arg Lys Asp His Leu Lys Asn His
920 65 70 75 80
922 Leu Gln Thr His Asp Pro Asn Lys Met Ala Phe Gly Cys Glu Glu Cys
923 85 90 95
925 Gly Lys Lys Tyr Asn Thr Met Leu Gly Tyr Lys Arg His Leu Ala Leu
926 100 105 110
928 His Ala Ala Ser Ser Gly Asp Leu Thr Cys Gly Val Cys Ala Leu Glu
929 115 120 125
931 Leu Gly Ser Thr Glu Val Leu Leu Asp His Leu Lys Ala His Ala Glu
932 130 135 140
934 Glu Lys Pro Pro Ser Gly Thr Lys Glu Lys Lys His Gln Cys Asp His
935 145 150 155 160
937 Cys Glu Arg Cys Phe Tyr Thr Arg Lys Asp Val Arg Arg His Leu Val
938 165 170 175
940 Val His Thr Gly Cys Lys Asp Phe Leu Cys Gln Phe Cys Ala Gln Arg
941 180 185 190
943 Phe Gly Arg Lys Asp His Leu Thr Arg His Thr Lys Lys Thr His Ser
944 195 200 205
946 Gln Glu Leu Met Lys Glu Ser Leu Gln Thr Gly Asp Leu Leu Ser Thr
947 210 215 220
949 Phe His Thr Ile Ser Pro Ser Phe Gln Leu Lys Ala Ala Leu Pro
950 225 230 235 240
952 Pro Phe Pro Leu Gly Ala Ser Ala Gln Asn Gly Leu Ala Ser Ser Leu
953 245 250 255
955 Pro Ala Glu Val His Ser Leu Thr Leu Ser Pro Pro Glu Gln Ala Ala
956 260 265 270
958 Gln Pro Met Gln Pro Leu Pro Glu Ser Leu Ala Ser Leu His Pro Ser
959 275 280 285
961 Val Ser Pro Gly Ser Pro Pro Pro Pro Leu Pro Asn His Lys Tyr Asn
962 290 295 300
964 Thr Thr Ser Thr Ser Tyr Ser Pro Leu Ala Ser Leu Pro Leu Lys Ala
965 305 310 315 320
967 Asp Thr Lys Gly Phe Cys Asn Ile Ser Leu Phe Glu Asp Leu Pro Leu
968 325 330 335
971 Gln Glu Pro Gln Ser Pro Gln Lys Leu Asn Pro Gly Phe Asp Leu Ala
972 340 345 350
974 Lys Gly Asn Ala Gly Lys Val Asn Leu Pro Lys Glu Leu Pro Ala Asp
975 355 360 365
977 Ala Val Asn Leu Thr Ile Pro Ala Ser Leu Asp Leu Ser Pro Leu Leu
978 370 375 380
980 Gly Phe Trp Gln Leu Pro Pro Pro Ala Thr Gln Asn Thr Phe Gly Asn

```

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/254,870

DATE: 07/12/2000  
 TIME: 14:07:01

Input Set : A:\52130apctus.app.txt  
 Output Set: N:\CRF3\07122000\I254870.raw

981	385				390				395				400
983	Ser	Thr	Leu	Ala	Leu	Gly	Pro	Gly	Glu	Ser	Leu	Pro	His
													Arg
													Leu
													Ser
984					405				410				415
986	Cys	Leu	Gly	Gln	Gln	Gln	Gln	Glu	Pro	Pro	Leu	Ala	Met
													Gly
													Thr
987					420				425				430
989	Ser	Leu	Gly	Gln	Leu	Pro	Leu	Pro	Pro	Ile	Pro	His	Val
													Phe
													Ser
990					435				440				445
992	Gly	Thr	Gly	Ser	Ala	Ile	Leu	Pro	His	Phe	His	His	Ala
													Phe
													Arg
993					450				455				460

E--> 994 96  
 E--> 998 14  
 E--> 1001 96

*delete*

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/254,870

DATE: 07/12/2000  
TIME: 14:07:02

Input Set : A:\52130apctus.app.txt  
Output Set: N:\CRF3\07122000\I254870.raw

L:12 M:220 C: Keyword misspelled or invalid format, [(F) ZIP:]  
L:18 M:220 C: Keyword misspelled or invalid format, [(F) ZIP:]  
L:25 M:220 C: Keyword misspelled or invalid format, [(v) COMPUTER READABLE FORM:]  
L:6 M:200 E: Mandatory Header Field missing, [(i) APPLICANT:] Value not provided  
L:0 M:200 E: Mandatory Header Field missing, [(A) ADDRESSEE:]  
L:0 M:248 E: Inserted missing Mandatory Header Field, [(iv) CORRESPONDENCE ADDRESS:]  
L:0 M:247 C: Inserted Optional Header Field, [(viii) ATTORNEY/AGENT INFORMATION:]  
L:0 M:249 C: Inserted Mandatory Field, [(vi) CURRENT APPLICATION DATA:]  
L:0 M:249 C: Inserted Mandatory Field, [(A) APPLICATION NUMBER:]  
L:0 M:249 C: Inserted Mandatory Field, [(B) FILING DATE:]  
L:50 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:1  
L:53 M:254 E: No. of Bases conflict, Input:0 Counted:110 SEQ:1  
L:56 M:254 E: No. of Bases conflict, Input:0 Counted:170 SEQ:1  
L:59 M:254 E: No. of Bases conflict, Input:0 Counted:230 SEQ:1  
L:62 M:254 E: No. of Bases conflict, Input:0 Counted:290 SEQ:1  
L:65 M:254 E: No. of Bases conflict, Input:0 Counted:350 SEQ:1  
L:68 M:254 E: No. of Bases conflict, Input:0 Counted:410 SEQ:1  
L:71 M:254 E: No. of Bases conflict, Input:0 Counted:470 SEQ:1  
L:74 M:254 E: No. of Bases conflict, Input:0 Counted:530 SEQ:1  
L:81 M:254 E: No. of Bases conflict, Input:0 Counted:634 SEQ:1  
L:82 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:84 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:86 M:254 E: No. of Bases conflict, Input:0 Counted:682 SEQ:1  
L:87 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:89 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:91 M:254 E: No. of Bases conflict, Input:0 Counted:730 SEQ:1  
L:92 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:94 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:96 M:254 E: No. of Bases conflict, Input:0 Counted:778 SEQ:1  
L:97 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:99 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:101 M:254 E: No. of Bases conflict, Input:0 Counted:826 SEQ:1  
L:102 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:104 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:106 M:254 E: No. of Bases conflict, Input:0 Counted:874 SEQ:1  
L:107 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:109 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:111 M:254 E: No. of Bases conflict, Input:0 Counted:922 SEQ:1  
L:112 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:114 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:116 M:254 E: No. of Bases conflict, Input:0 Counted:970 SEQ:1  
L:117 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:119 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:121 M:254 E: No. of Bases conflict, Input:0 Counted:1018 SEQ:1  
L:122 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:124 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:126 M:254 E: No. of Bases conflict, Input:0 Counted:1066 SEQ:1  
L:127 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1

7/12/00

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/254,870DATE: 07/12/2000  
TIME: 14:07:02Input Set : A:\52130apctus.app.txt  
Output Set: N:\CRF3\07122000\I254870.raw

L:129 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:131 M:254 E: No. of Bases conflict, Input:0 Counted:1114 SEQ:1  
L:132 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:134 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:136 M:254 E: No. of Bases conflict, Input:0 Counted:1162 SEQ:1  
L:137 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:139 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:141 M:254 E: No. of Bases conflict, Input:0 Counted:1210 SEQ:1  
L:142 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:144 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:147 M:254 E: No. of Bases conflict, Input:0 Counted:1258 SEQ:1  
L:148 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:150 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:152 M:254 E: No. of Bases conflict, Input:0 Counted:1306 SEQ:1  
L:153 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:155 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:157 M:254 E: No. of Bases conflict, Input:0 Counted:1354 SEQ:1  
L:158 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:160 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:162 M:254 E: No. of Bases conflict, Input:0 Counted:1402 SEQ:1  
L:163 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:165 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:167 M:254 E: No. of Bases conflict, Input:0 Counted:1450 SEQ:1  
L:168 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:170 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:172 M:254 E: No. of Bases conflict, Input:0 Counted:1498 SEQ:1  
L:173 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:175 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:177 M:254 E: No. of Bases conflict, Input:0 Counted:1546 SEQ:1  
L:178 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:180 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:182 M:254 E: No. of Bases conflict, Input:0 Counted:1594 SEQ:1  
L:183 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:185 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:187 M:254 E: No. of Bases conflict, Input:0 Counted:1642 SEQ:1  
L:188 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:190 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:192 M:254 E: No. of Bases conflict, Input:0 Counted:1690 SEQ:1  
L:193 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:195 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:197 M:254 E: No. of Bases conflict, Input:0 Counted:1738 SEQ:1  
L:198 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:200 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:202 M:254 E: No. of Bases conflict, Input:0 Counted:1786 SEQ:1  
L:203 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:205 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:207 M:254 E: No. of Bases conflict, Input:0 Counted:1834 SEQ:1  
L:208 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:210 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1



VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/254,870

DATE: 07/12/2000  
TIME: 14:07:02

Input Set : A:\52130apctus.app.txt  
Output Set: N:\CRF3\07122000\I254870.raw

L:212 M:254 E: No. of Bases conflict, Input:0 Counted:1882 SEQ:1  
L:213 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:215 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:217 M:254 E: No. of Bases conflict, Input:0 Counted:1930 SEQ:1  
L:218 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:220 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:223 M:254 E: No. of Bases conflict, Input:0 Counted:1978 SEQ:1  
L:224 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:226 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:228 M:254 E: No. of Bases conflict, Input:0 Counted:2026 SEQ:1  
L:229 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:231 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:233 M:254 E: No. of Bases conflict, Input:0 Counted:2074 SEQ:1  
L:234 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:236 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:238 M:254 E: No. of Bases conflict, Input:0 Counted:2122 SEQ:1  
L:239 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:241 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:243 M:254 E: No. of Bases conflict, Input:0 Counted:2170 SEQ:1  
L:244 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:246 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:248 M:254 E: No. of Bases conflict, Input:0 Counted:2218 SEQ:1  
L:249 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:251 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:253 M:254 E: No. of Bases conflict, Input:0 Counted:2266 SEQ:1  
L:254 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:256 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:258 M:254 E: No. of Bases conflict, Input:0 Counted:2314 SEQ:1  
L:259 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:261 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:263 M:254 E: No. of Bases conflict, Input:0 Counted:2362 SEQ:1  
L:264 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:266 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:268 M:254 E: No. of Bases conflict, Input:0 Counted:2410 SEQ:1  
L:269 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:271 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:273 M:254 E: No. of Bases conflict, Input:0 Counted:2458 SEQ:1  
L:274 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:276 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:278 M:254 E: No. of Bases conflict, Input:0 Counted:2506 SEQ:1  
L:279 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:281 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:283 M:254 E: No. of Bases conflict, Input:0 Counted:2555 SEQ:1  
L:284 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:286 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:288 M:254 E: No. of Bases conflict, Input:0 Counted:2605 SEQ:1  
L:291 M:254 E: No. of Bases conflict, Input:0 Counted:2665 SEQ:1  
L:294 M:254 E: No. of Bases conflict, Input:0 Counted:2725 SEQ:1  
L:297 M:254 E: No. of Bases conflict, Input:0 Counted:2785 SEQ:1

7/12/00

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/254,870

DATE: 07/12/2000  
TIME: 14:07:02Input Set : A:\52130apctus.app.txt  
Output Set : N:\CRF3\07122000\I254870.raw

L:436 M:342 E: Invalid Stop Code On Error, STOP CODON:\*

L:542 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7

L:701 M:254 E: No. of Bases conflict, Input:0 Counted:50 SEQ:16

L:704 M:254 E: No. of Bases conflict, Input:0 Counted:110 SEQ:16

L:707 M:254 E: No. of Bases conflict, Input:0 Counted:170 SEQ:16

L:710 M:254 E: No. of Bases conflict, Input:0 Counted:230 SEQ:16

L:713 M:254 E: No. of Bases conflict, Input:0 Counted:290 SEQ:16

L:716 M:254 E: No. of Bases conflict, Input:0 Counted:350 SEQ:16

L:719 M:254 E: No. of Bases conflict, Input:0 Counted:410 SEQ:16

L:722 M:254 E: No. of Bases conflict, Input:0 Counted:470 SEQ:16

L:725 M:254 E: No. of Bases conflict, Input:0 Counted:530 SEQ:16

L:728 M:254 E: No. of Bases conflict, Input:0 Counted:590 SEQ:16

L:731 M:254 E: No. of Bases conflict, Input:0 Counted:650 SEQ:16

L:734 M:254 E: No. of Bases conflict, Input:0 Counted:710 SEQ:16

L:737 M:254 E: No. of Bases conflict, Input:0 Counted:770 SEQ:16

L:740 M:254 E: No. of Bases conflict, Input:0 Counted:832 SEQ:16

L:741 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16

L:745 M:254 E: No. of Bases conflict, Input:0 Counted:880 SEQ:16

L:746 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16

L:748 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16

L:750 M:254 E: No. of Bases conflict, Input:0 Counted:928 SEQ:16

L:751 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16

L:753 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16

L:755 M:254 E: No. of Bases conflict, Input:0 Counted:976 SEQ:16

L:756 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16

L:758 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16

L:760 M:254 E: No. of Bases conflict, Input:0 Counted:1024 SEQ:16

L:761 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16

L:763 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16

L:765 M:254 E: No. of Bases conflict, Input:0 Counted:1072 SEQ:16

L:766 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16

L:768 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16

L:770 M:254 E: No. of Bases conflict, Input:0 Counted:1120 SEQ:16

L:771 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16

L:773 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16

L:775 M:254 E: No. of Bases conflict, Input:0 Counted:1168 SEQ:16

L:776 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16

L:778 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16

L:780 M:254 E: No. of Bases conflict, Input:0 Counted:1216 SEQ:16

L:781 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16

L:783 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16

L:785 M:254 E: No. of Bases conflict, Input:0 Counted:1264 SEQ:16

L:786 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16

L:788 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16

L:790 M:254 E: No. of Bases conflict, Input:0 Counted:1312 SEQ:16

L:791 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16

L:793 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16

L:795 M:254 E: No. of Bases conflict, Input:0 Counted:1360 SEQ:16

L:796 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/254,870

DATE: 07/12/2000  
TIME: 14:07:02

Input Set : A:\52130apetus.app.txt  
Output Set: N:\CRF3\07122000\I254870.raw

L:798 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16  
L:800 M:254 E: No. of Bases conflict, Input:0 Counted:1408 SEQ:16  
L:801 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16  
L:803 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16  
L:805 M:254 E: No. of Bases conflict, Input:0 Counted:1456 SEQ:16  
L:806 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16  
L:808 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16  
L:810 M:254 E: No. of Bases conflict, Input:0 Counted:1504 SEQ:16  
L:811 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16  
L:813 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16  
L:815 M:254 E: No. of Bases conflict, Input:0 Counted:1552 SEQ:16  
L:816 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16  
L:818 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16  
L:820 M:254 E: No. of Bases conflict, Input:0 Counted:1600 SEQ:16  
L:821 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16  
L:823 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16  
L:825 M:254 E: No. of Bases conflict, Input:0 Counted:1648 SEQ:16  
L:826 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16  
L:828 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16  
L:830 M:254 E: No. of Bases conflict, Input:0 Counted:1696 SEQ:16  
L:831 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16  
L:833 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16  
L:835 M:254 E: No. of Bases conflict, Input:0 Counted:1744 SEQ:16  
L:836 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16  
L:838 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16  
L:840 M:254 E: No. of Bases conflict, Input:0 Counted:1792 SEQ:16  
L:841 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16  
L:843 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16  
L:845 M:254 E: No. of Bases conflict, Input:0 Counted:1840 SEQ:16  
L:846 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16  
L:848 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16  
L:850 M:254 E: No. of Bases conflict, Input:0 Counted:1888 SEQ:16  
L:851 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16  
L:853 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16  
L:855 M:254 E: No. of Bases conflict, Input:0 Counted:1936 SEQ:16  
L:856 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16  
L:858 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16  
L:860 M:254 E: No. of Bases conflict, Input:0 Counted:1984 SEQ:16  
L:861 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16  
L:863 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16  
L:865 M:254 E: No. of Bases conflict, Input:0 Counted:2032 SEQ:16  
L:866 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16  
L:868 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16  
L:870 M:254 E: No. of Bases conflict, Input:0 Counted:2080 SEQ:16  
L:871 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16  
L:873 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16  
L:875 M:254 E: No. of Bases conflict, Input:0 Counted:2128 SEQ:16  
L:876 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16  
L:878 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16

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## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/254,870

DATE: 07/12/2000

TIME: 14:07:02

Input Set : A:\52130apctus.app.txt

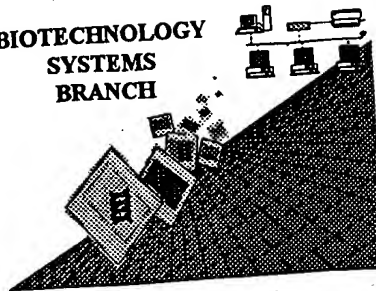
Output Set: N:\CRF3\07122000\I254870.raw

L:880 M:254 E: No. of Bases conflict, Input:0 Counted:2176 SEQ:16  
L:881 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16  
L:883 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16  
L:887 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16  
L:889 M:254 E: No. of Bases conflict, Input:0 Counted:2272 SEQ:16  
L:892 M:254 E: No. of Bases conflict, Input:0 Counted:2334 SEQ:16  
L:893 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16  
L:994 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17  
L:998 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17  
L:1001 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17

Patterson

no

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



#9

## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/254,870

Source: 1652

Date Processed by STIC: 7/12/2000

RECEIVED

JUL 28 2000

TECH CENTER 1600/2800

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY  
EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER,  
703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW:

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25. Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:  
<http://www.uspto.gov/web/offices/pac/checker>